

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:42:01 ; Search time 77.81 Seconds

(without alignments)
291.208 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277
Sequence: 1 MKRFSORLEPGPSYONIKS.....LRKPCICGIIKGTVFELS 618

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3277	100.0	618	1	BIR3_HUMAN
2	2728	83.2	612	1	BIR3_MOUSE
3	2353	71.8	604	1	BIR2_HUMAN
4	2233.5	68.2	611	1	BIR2_CHICK
5	2172	66.3	600	1	BIR2_MOUSE
6	1532	46.8	358	1	PIAP_PIG
7	911	27.8	497	1	BIR4_HUMAN
8	910	27.6	496	1	BIR4_MOUSE
9	904.5	27.6	496	1	BIR4_RAT
10	744.5	22.7	498	1	IAP2_DROME
11	513	15.7	268	1	IAP3_NPVOP
12	506	15.4	1403	1	BIR6_MOUSE
13	499.5	15.2	1403	1	BIR6_MOUSE
14	498.5	15.2	1402	1	BIR6_MOUSE
15	484	14.8	438	1	IAP1_DROME
16	468.5	14.3	1403	1	BIRA_MOUSE
17	468	14.3	1447	1	BIRB_MOUSE
18	462	14.1	1403	1	BIR1_HUMAN
19	461	14.1	1403	1	IAP1_HUMAN
20	238.5	7.3	286	1	IAP1_NPVAC
21	237.5	7.2	997	1	BIR1_SCHPO
22	223.5	6.8	275	1	IAP1_NPVOP
23	199.5	6.1	4829	1	BIR6_HUMAN
24	175.5	5.4	239	1	ZFP_TRY6
25	144	4.4	249	1	IAP2_NPVAC
26	141.5	4.3	142	1	BIR5_RAT
27	139	4.2	140	1	BIR5_MOUSE
28	137.5	4.2	236	1	IAP2_NPVOP
29	132.5	4.0	480	1	MDK4_HUMAN
30	131	4.0	142	1	BIR5_HUMAN
31	126	3.8	142	1	ZER2_TRY6
32	120.5	3.7	834	1	TNC4_CAEEL
33	120.5	3.7	934	1	BIR1_YEAST

34	119.5	3.6	487	1	MDK2_CANFA
35	119.5	3.6	735	1	YD07_SCHPO
36	119	3.6	619	1	PR1A_HELPY
37	116.5	3.6	3418	1	BRC2_HUMAN
38	116	3.5	624	1	YMO8_YEAST
39	115.5	3.5	491	1	MDK2_HUMAN
40	112.5	3.4	1075	1	PSY2_SCHPO
41	112.5	3.4	1138	1	DP52_YEAST
42	109	3.3	619	1	PR1A_HELPY
43	109	3.3	1969	1	PR1A_CAEEL
44	109	3.3	2351	1	FAB_HUMAN
45	109	3.3	2469	1	TEDU_HVSA

ALIGNMENTS

RESULT 1
ID BIR3_HUMAN STANDARD; PRT: 618 AA.
AC Q13450: Q16516; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IN REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS
DE PROTEIN 2) (H1AP2) (H1AP-2) (C-1AP1) (TNFR2-TNFR SIGNALING COMPLEX
DE PROTEIN 2) (H1AP2 OR H1AP2 B).
OS Homo sapiens (Human).
GN BIR3 OR A12 OR IAP2 OR M1HB.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP MEDLINE=96128127; PubMed=8548810;
RA Rother M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFR signaling complex contains two novel proteins related
RL Cell 83:1243-1252(1995).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96149249; PubMed=8552191;
RX Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,
RA Parahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RL family of IAP genes.";
RN Nature 379:349-353(1996).
[3]
RP SEQUENCE FROM N.A.
RA MEDLINE=96209843; PubMed=8643514;
RX Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;
RA "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RL receptor-associated factors.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
[4]
RP STRUCTURE BY NMR OF 266-363
RA MEDLINE=99332054; PubMed=10404221;
RX Hinde M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RL repeat.";
RN Mol. Struct. Biol. 6:648-651(1999).
[5]
RP FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC SUBCELLULAR LOCATION: CYTOSOL; CYTOSOL (POTENTIAL).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
LEUKOCYTES.
CC

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CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: I49433; AAC1942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37347; AAC50508.1; -
DR FDB: 10BH; 20-OCT-99.
DR MIR: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
KM Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 539 CARD.
FT ZN_FING 571 605 CARD.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> M (IN REF. 2).
SO SEQUENCE 618 AA: 69899 MW: 117780328053660 CMC64;

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Query Match 100.0%; Score 3277; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 1,2e-212;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHKTSQRLEFGPSYONIKSIMEDSTILSDMTNSMKKKYDFSCELYRMSTYTFPGYV 60
DB 1 MHKTSQRLEFGPSYONIKSIMEDSTILSDMTNSMKKKYDFSCELYRMSTYTFPGYV 60
QY 61 PVSERSIARAGFYTYGVNDKKYCCGCLMDNMKLGDSPTQKHOLYPCSCFTQNLVAS 120
DB 61 PVSERSIARAGFYTYGVNDKKYCCGCLMDNMKLGDSPTQKHOLYPCSCFTQNLVAS 120
QY 121 LGSTSKNTSPRNSFAHSLPTLEHSSLFGSYSSLSPPNLSRAVEDISSRTPYSYA 180
DB 121 LGSTSKNTSPRNSFAHSLPTLEHSSLFGSYSSLSPPNLSRAVEDISSRTPYSYA 180
QY 121 LGSTSKNTSPRNSFAHSLPTLEHSSLFGSYSSLSPPNLSRAVEDISSRTPYSYA 180
DB 121 LGSTSKNTSPRNSFAHSLPTLEHSSLFGSYSSLSPPNLSRAVEDISSRTPYSYA 180
QY 181 MSTEERFLUTYHMMPLTFLSPSELARAGFYTYGCGDVACFCACGKLSMNEPKDAMSEH 240
DB 181 MSTEERFLUTYHMMPLTFLSPSELARAGFYTYGCGDVACFCACGKLSMNEPKDAMSEH 240
QY 241 RHRFPKCFLENSLETLPSTISNLSMOTHAARMFTFWYPPSSVYPOEOLASAGFYVGR 300
DB 241 RHRFPKCFLENSLETLPSTISNLSMOTHAARMFTFWYPPSSVYPOEOLASAGFYVGR 300
QY 301 NDVYKCCGCGGCLRCWEGGDDPMVYHAKKFPKCFELRLKKGGEYDEIQCRPHLLDQL 360
DB 301 NDVYKCCGCGGCLRCWEGGDDPMVYHAKKFPKCFELRLKKGGEYDEIQCRPHLLDQL 360
QY 361 STSDTTEGNADPPIIHGCPRESSSEDVAMKNTVYKASLEKGNRDLAKOTVOSKILTT 420
DB 361 STSDTTEGNADPPIIHGCPRESSSEDVAMKNTVYKASLEKGNRDLAKOTVOSKILTT 420

DB 361 STSDTTEGNADPPIIHGCPRESSSEDVAMKNTVYKASLEKGNRDLAKOTVOSKILTT 420
QY 421 GENYKTVNDIYSLALNAEDEREKEEKEKADEMASSDLSLTKNNMALPQOITCYLPILD 480
DB 421 GENYKTVNDIYSLALNAEDEREKEEKEKADEMASSDLSLTKNNMALPQOITCYLPILD 480
QY 481 MLKANVINKEOHDITIKOTIPLQARELITPLIVYKMAANIRKNCLEIDSTLYKNLP 540
DB 481 MLKANVINKEOHDITIKOTIPLQARELITPLIVYKMAANIRKNCLEIDSTLYKNLP 540
QY 541 VDKNNKTYPTEDVSGSLSEBQLRRHQEERTKVCMDKEVSVYFIPCGHLVWCQECAPSLR 600
DB 541 VDKNNKTYPTEDVSGSLSEBQLRRHQEERTKVCMDKEVSVYFIPCGHLVWCQECAPSLR 600
QY 601 KCPICGILKGTVPRTLS 618
DB 601 KCPICGILKGTVPRTLS 618

RESULT 2
ID BIR3_MOUSE STANDARD: PRT: 612 AA.
AC 062210; 008864;
DT 01-NOV-1997 (Ref. 35, Created)
DT 01-NOV-1997 (Ref. 35, Last sequence update)
DT 20-AUG-2001 (Ref. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS
DE PROTEIN 2) (MIAP2) (MIAP-2).
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxId=10090;
RX MEDLINE=96128127; PubMed=8548810;
RT "The TNFR2-TNFR1 signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RN Cell 83:1243-1252(1995).
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RT Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: I49433; AAC2078.1; -
DR EMBL: U88909; AAC3532.1; -
DR MCD: MG1:1197009; BIR3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.

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550 TEVSLSLSEDLRLRLOEPRFCVCKDEKVEVFIPCHLWVCEQACSLKRCIORCI 609
Db 532 TDIDIALMHEMDLRKLOEERKVCVCKDEKVEVFIPCHLWVCEQACSLKRCIORCI 591
Qy 610 KGVTRFFLS 618
Db 592 KGVTRFFLS 600

RESULT 6
PIAP.PIG STANDARD: PRT: 358 AA.
ID PIAP.PIG
AC 062640:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUNITIVE INHIBITOR OF APOPTOSIS.
PIAP
NC SUE SCROFA (PIG).
OS EUTEROPOA: METAZOA: CHORDATA: CRANIATA: VERTEBRATA: EUTELIOSCOMI:
OC Mammalia: Eubacteria: Cetartiodactyla: Suina; Suidae; Sus.
NCML_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98162622; PubMed=501011;
RX Stehlik C., de Martin R., Binder B.R., IAPP J.;
RA "Cytokine induced expression of pore-forming inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B."
RL Biochem Biophys Res Commun 243:827-832(1998).
CC -1 SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1 SIMILARITY: CONTAINS 2 IAP REPEATS.
CC -1 SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC EMBL: U79142; AAC39171.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001335; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR_2.
DR Pfam: PF00619; CARD_1.
DR Pfam: PF00997; zfc3HC4_1.
DR SMART: SM00238; BIR_2.
DR SMART: SM00114; CARD_1.
DR SMART: SM00164; RING_1.
DR PROSITE: PS01262; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS0209; CARD_1.
DR Apoc2o1s; zinc_finger; Repeat.
DR Apoc2o1s; zinc_finger; BIR_1.
DR Repeat 90 157
DR Repeat 311 345 RING-TYPE
FT ZN_FING 358 AA; 4097 MW; EBI268F9A619004 CRC64;
SQ SEQUENCE 358 AA;

Query Match 46 88; Score 1532; DB 1; Length 358;
Best Local Similarity 65.1%; Freq. No. 7, 8e-96;
Matches 286; Conservative 36; Mismatches 33; Indels 82; Gaps 2

OY 181 MSTEENARFLITWMPPLTFLSPSELNAGYYITGCGDRAVCACGCGKLSMWEKDDAMSH 240
Db 1 MNTKORLTLTFOMPPLTFLSPDLAKAGYYITGCGDRAVCACGCGKLSMWEKDDAMSH 60
OY 241 RRRFPNCPFLNSL-ETLTFSTISLMSQTHARKRTFMPWSSVVPDPRDLASAGYYIVG 299

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Db	Accession	Gene	Protein	Length
Db	61	LRHHPNCPPLNQGLQDSRYTNSIKQTYAARFETPCNMPSSIPVHPFOLASAGFYTG	120	359
Qy	300	RNDVDFCFCCGCGJRCWSEGGDDPWVYHAKKPRCFELIRKMGGEFVDEIGRRPHLLFOL	120	359
Db	121	HSDDVCFCCGCGJRCWSEGGDDPWVYHAKKPRCFEYLIRKMGGEFISHVQASYPHLLFOL	120	180
Qy	360	LSTDVGTGGENAADPPIIHFGPCESSSDAVMNPTPVYKSALEMGFNBDLYKQTVOSKILTF	120	419
Db	181	LSTDSDPDENAEAPP	120	155
Qy	420	TGENYTVNDIVSALMADEKREBEKQAEEMASDLSLIRKNMMLFQOOLTCVPL	120	479
Db	196	-----NDLSLIRKNMMLFQOOLTCVPL	120	219
Qy	480	DILKKANVINKGEDIHKQKTOPLQARELPIITLVKGNMAAFKRLCLKEIDSTLYRNL	120	539
Db	220	DSLIIARVISEGDEHDVKKQTSLOARELITLILVKGNAATFKNSLQEDIDPMYKRL	120	279
Qy	540	FVDSKNKTYIPFDDVSGSLSEBDDLRLOEBPTCKVCMDEKVSVVFIPCGHLYVQCEASL	120	539
Db	280	FVQDDIKRIPTEBNVSDLSMQRRLQREPTCKVCMDEKVSIVFIPCGHLYVQCDASL	120	339
Qy	600	RKPCIGRIGIKQVTRFLS 618	120	618
Db	340	RKPCIGRIGIKQVTRFLS 358	120	358
RESULT 7				
ID	BIR4_HUMAN	STANDARD:	PRT:	497 AA.
AC	P98170: Q9NO14:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS PROTEIN 3) (X-LINKED IAP)			
DE	(IAP-LIKE PROTEIN) (HLLP).			
GN	BIR4 OR AIP3 OR IAP3 OR XIAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CC	NCBI_TaxID=9606;			
SC	SEQUENCE FROM N.A.			
RP	TISSUE=Retal brain;			
RC	MEDLINE=96149249: Pubmed=8552191;			
RX	Lifton P., Roy N., Tamai K., Lefebvre C., Baird S., Chertion-Horvat G.,			
RA	Fairbank R., McLean M., Ikeda J., Macchensz A., Korneluk R.G.;			
RA	*Suppression of apoptosis in mammalian cells by NAIP and a related			
RT	family of IAP genes".			
RL	Nature 379:349-353(1996).			
RN	[1]			
SC	SEQUENCE FROM N.A.			
RP	TISSUE=Retal heart;			
RC	MEDLINE=9625286: Pubmed=8654366;			
RX	Duckett C.S., Naya V.E., Gedrich R.M., Clem R.J., van Dongen J.L.,			
RA	Guilligan M.C., Shields H., Hardwick J.M., Thompson C.B.;			
RA	*A conserved family of cellular genes related to the baculovirus Iap			
RT	gene and encoding apoptosis inhibitors".			
RL	EMBO J. 15:2685-2694(1996).			
RN	[3]			
SC	SEQUENCE FROM N.A.			
RP	Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.			
RL	[4]			
FUNCTION				
RX	MEDLINE=97373959: Pubmed=9230442:			
RA	Deaux O.L., Takahashi R., Saljeen G.S., Reed J.C.;			
RA	*X-linked IAP is a direct inhibitor of cell-death proteases".			
RL	Nature 383:300-304(1997).			
CC	-1- EDUCATION; APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND			
CC	CASPASE-7.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			


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FT CONFLICT 322 322 M -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SO SEQUENCE 496 AA; 56079 MM; EC5FA0799F2CC0D8 CAC64;

Query Match 27.8% Score 910; DB 1; Length 496;
Best Local Similarity 32.5%; Pred. No. 7e-54;
Matches 203; Conservative 92; Mismatches 156; Indels 174; Gaps 14;

OY 27 ILSDMNSKKKMKYDFSCELYRMSYTFPPAGVSESLARACFYTGVDKXKCC 86
DB 13 VLND--TKDE--EVEEFNRKLTANFPSSVSASTLAKAFLYTGSDTQVCSG 66
OY 87 GLMDMMKLGSPLOKHOLYPCSPFTONLVASLSTSKNTSPRNSFANSLPTLEHS 146
DB 67 HAALDMQYGSAAVGRHRIRISNCRFT-----NGTFENGGAOSTNFGIQNG 113
OY 147 SLFS---GSYSLSPNP-----LMSRAVEDISSSTNPVSAMTEARFLTYHM 193
DB 114 QYSENGCVNNPPADRPPEPTHADYLLTQGVVDISDT-TPRNPAMCSBARLKSFON 172
OY 194 WP-LTFLSBELARAGFYIGPGRVACFACGKLSNMEPKDAMSEHRRHFPNCPL- 250
DB 173 WPOYAHLPRELASAGLYTGADDOVCCCGCKLEMMFPCDRAMSEHRRHFPNCFLVG 232
OY 251 -----ENSLFTRFSISNLSMOTHAARKTFYWPSSVPOPPOLASA 293
DB 233 RNYNVSESGVSDRNPSTNSPR---NPMAEYVARLYTFEGTWISS--VAKDOLARA 286
OY 294 GFYYVGRNDVYKFCDCGGLRCWESGDDPMVYHAKMPEPCDFELIMKGFPEVDEIGRYP 353
DB 287 GFVALDEGKCFKFCGGLTDMKPEDEPWOHAKMYPCGCKYLLDEGGEYIINI----- 341
OY 354 HLEQOLSTSDTGEENADPRLIHFGSGSSSEDAVMNTPVAKSALEMFNPNDLYKQTV 413
DB 342 HLHSLSELSLGRTEKT-----PSLTKRIDTDTFQNPVYQALIRMGFSRDKITM 392
OY 414 QSKILTEGNTKYNDIVSALINADKREEREKQAEKMASSDLSLRKNMALFQOLT 473
DB 393 EKKIQTSGSYSLLEVLIADLVSAQKNTED----- 424
OY 474 CVLPIDNLKANVINKOEHDIKOKTOLPILOABELDTILVKKMAANFKKCKAIEDS 533
DB 425 -----SSQTSID----- 431
OY 534 TLVKNLPVDNKKMKTPEEDVSGLSLEQOLRLQDERCKAYCDKVSVAITPCGLVYCO 593
DB 432 -----KDISTEOLARRLOEKCKLCKMDRNIATVPEVCHGLVYCK 471
OY 594 ECAPSLKRCPLICRGIIKGTVPFLS 618
DB 472 QCAEAVDKCPMCKVTITFKOKIFMS 496

RESULT 9
BIR4_RAT STANDARD: PRT; 496 AA.
AC Q9R016;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS
DE PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)
DE (IAP HOMOLOG A) (RIAP3) (RIAP-3).
GN BIR4 OR AIP3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RA SEQUENCE FROM N.A.
RA Saito N.;
FT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND
CC -1- CASPASE-7 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL;SMC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC
DR EMBL; AB033366; BAA85304.1; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR Apoptosis; Zinc-finger; Repeat.
KW * REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 1.
FT REPEAT 264 329 BIR 2.
FT ZN_FING 449 483 RING-TYPE.
FT SEQUENCE 496 AA; 56072 MM; E250B3C7461A469 CRC64;

Query Match 27.6% Score 904.5; DB 1; Length 496;
Best Local Similarity 33.2%; Pred. No. 1.6e-53;
Matches 206; Conservative 86; Mismatches 155; Indels 173; Gaps 15;

OY 33 NSNKKMKYDFSCELYRMSYTFPPAGVSESLARACFYTGVDKXKCCGLMDLN 92
DB 16 DTKDE--EVEEFNRKLTANFPSSVSASTLAKAFLYTGSDTQVCSGHAVDR 72
OY 93 WKLGSPLOKHOLYPCSPFTONLVASLSTSKNTSP-----MNSRANHS 138
DB 73 WQYGSAAVGRHRIRISNCRFTINGFTEN-GAT-QTSPIQONGQYSENGCVNNRRA-- 128
OY 139 LSEFLHSSLPSSGSYSLSLSPNPINSRAVBDISSRTNPTVAMSTEBARFLTYHMP-LT 197
DB 129 ---LDRSETIADYL-----LRTGVVDISDT-TPRNPAMCSBARLKTFQWPDYA 177
OY 198 FLSPBELARAGFYIGPGRVACFACGKLSNMEPKDAMSEHRRHFPNCPL----- 250
DB 178 HLSPELRLASAGLYTGIDDOVCCCGCKLNMPEPCDRAMSEHRRHFPNCFLVGRVNV 237
OY 251 -----ENSLFTRFSISNLSMOTHAARKTFYWPSSVPOPPOLASAGFYV 298
DB 238 RSESGVSDRNPSTNSPR---NPMAEYVARLYTFEGTWISS--VAKDOLARA 286
OY 299 GRNDVYKFCDCGGLRCWESGDDPMVYHAKMPEPCDFELIRMKGOEFDVDEIGRYPHLLEQ 358
DB 292 GEEDVYKFCFCGGLTDMKPEDEPWOHAKMYPCGCKYLLDEGGEYIINI-----HLHIS 346
OY 359 LLSDDTTEGEMADPRLIHFGSGSSSEDAVMNTPVAKSALEMFNPNDLYKQVOSKTL 418
DB 347 LGEYSVTRAKET-----PSYTKRIDTDTFQNPVYQALIRMGFSRDKITMCKEIQ 397
OY 419 TGGBNKYNDIVSALINADKREEREKQAEKMASSDLSLRKNMALFQOLTCVLP 478

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QY 533 STLYKNLFVDKNNKIPTEDVSGLSLEBOJRLQOEPTCKNCKMEKVSVPYIPGCHLYNC 592
 DB 215 -----VADRLICATLGAERTVCFPCGVAC 242
 QY 593 QCCASLRKCPICGICGIIKTVRTF 616
 DB 243 GKCAGAVTTCVCRQGLDKAVMAY 266
 RESULT 12
 BIRF_MOUSE STANDARD: PRT: 1403 AA.
 ID BIRF_MOUSE Q8R029, P81703: 009122: 009121:
 AC Q8R016: Q8R029, P81703: 009122: 009121:
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1E (NEURONAL APOPTOSIS
 GN INHIBITOR PROTEIN 5)
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99431676; PubMed=10501978;
 RA Huang S., Schaff J.M., Gromney J.D., Endrizzi M.G., Dietrich W.F.;
 RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
 RT functional transcripts." (1999).
 RL Mamm. Genome 10:1032-1035(1999).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=128/SV;
 RA Endrizzi M., Huang S., Schaff J.M., Kelter A.R., Wirth B.,
 RA Kunkel L.M., Miller W., Dietrich W.F.;
 RT "Comparative sequence analysis of the mouse and human Nalp5/MA
 RT interval." (1999).
 RL Genomics 60:137-151(1999).
 RN 131
 RP SEQUENCE OF 82-168 FROM N.A.
 RC STRAIN=129/SV;
 RA MEDLINE=97131520; PubMed=8975718;
 RA Schaff J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
 RA Kunkel L.M., Dietrich W.F.;
 RT "The mouse region syntenic for human spinal muscular atrophy lies
 RT within the Nalp critical interval and contains multiple copies of
 RT exon 5." (1999).
 RL Genomics 38:405-417(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DB EMBL: AF135492; AAD56764.1; -;
 DB EMBL: AF131205; AAD56760.1; -;
 DB EMBL: U66326; AAC52974.1; -;
 DB MGD: MGI:1298220; Bircle.
 DB InterPro: IPR001370; BIR.
 DB Pfam: PF00653; BIR; 3.
 DB SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.

FT REPEAT 278 345 BIR 3.
 FT CONFLICT 92 92 K -> R (IN REF. 1).
 FT CONFLICT 144 144 S -> R (IN REF. 1).
 FT CONFLICT 242 242 S -> G (IN REF. 2).
 FT CONFLICT 472 472 T -> A (IN REF. 2).
 FT CONFLICT 516 516 A -> A (IN REF. 2).
 FT CONFLICT 521 521 Y -> T (IN REF. 2).
 FT CONFLICT 533 533 Y -> A (IN REF. 2).
 FT CONFLICT 538 538 S -> A (IN REF. 2).
 FT CONFLICT 1092 1092 E -> I (IN REF. 2).
 FT CONFLICT 1126 1126 H -> L (IN REF. 2).
 FT CONFLICT 1137 1137 H -> Q (IN REF. 2).
 FT CONFLICT 1242 1242 Y -> Q (IN REF. 2).
 FT CONFLICT 1276 1276 D -> N (IN REF. 2).
 FT SEQUENCE 1403 AA; 159695 MW; 5275645043RCED42 CRC64;
 SO
 Query Match 15.4%, Score 506, DB 1; Length 1403;
 Best Local Similarity 27.3%, Pred. No. 3, 9e-26;
 Matches 179; Conservative 179; Mismatches 216; Indels 176; Gaps 27;
 QY 14 STONKSTWEDSTLSDWNSNKKKKNDPSCF-----LYNNTSTTFPAGYVPSERS 66
 DB 31 AFVAKSOEER-----HKRNKKKKKQFNDSORSEARLRTFTETDTFRSWTF---OE 80
 QY 67 IARAGPYTYGVNDKYKCFCCGJLMDNKKLGDSPIQKHQDLPSCSFIONLYASLSSTSK 126
 DB 81 MAAAGFYHGVAGLVQCFCCSLILGNSLRKLPLEKHKLPBCEFLQ---GKDVGNCK 137
 QY 127 KTSFMRKSTMSLSPLTBHSIFSGSYSSLSPNPLNSRAVEDJSSSTHTPYSYMASTDEA 186
 DB 138 IDIRK-----SPEM-----LRGKARY--HEERA 161
 QY 187 RFLTYHMKPLTF--LSPSLARAGPYTYIGDGRVACAGCGKLSNWPEDDMSFNRRF 244
 DB 162 RLSFSEDFWTFYAHGTSRYVLSAGAFYTKROYQCRSCGSLGAKMAEDDDMKRFFP 221
 QY 245 PNCFFLEL--SLETLRFSTISNLSMOTHA-----R 272
 DB 222 PCECELSKSSSEELAQITOSTEGFVYVGHGFYKSKYRELPVAYKACNDSPVANEER 281
 QY 273 MEFPMYPSVPVOPPOLASAGFYVGRNDYKCFCCDGLRCWESGDPPWEAKKFFR 332
 DB 282 KMFRMDPESVGEVALVRAGEFYTKDKDIKRCSCGGLKMAEDDDMKRFFP 341
 QY 333 CEFLIRKQ--EVDDELGRYPHLLRDLSTSDTTGREN--ADPPIH----- 377
 DB 342 CVFLQTLKSSAELVPLTLOSQY-----ALPEATETRESNHGDAAVSTVVDLGRSPAQ 396
 QY 378 FQPESSSEDA-----VMNTPVYKSAI-----EMGKNRDLKQVOSKILTF 420
 DB 397 FEENRSLSTGLNDYTKATFRHMNIPEVCSLGDHLLSCDVSITSNHSISOV--EALVI 455
 QY 421 GENKYTVNDIVSALLNAEDKREER--EKOAEEMASDLSLIRKRNALFOOLTCVLP 477
 DB 456 PVEYSNLSNVMK-----VEGETSGRTFKRLAFLAMSGCLLYRRQLFLSLSSITP 511
 QY 478 IIDNLLAVNYIKQEHDIKQKTOPLQARELIDTLTVKGNMAANIFKNCI--KEIDSTLY 536
 DB 512 --DGL--ANITQ-------LLGAGGCSISV--CLASSITQQLQH 544
 QY 537 KNLFDVKNKKKIPTEDVSGI--SLEBOJRLQOE-----PTC 571
 DB 545 QVLEP-----LDVYSGLSASTFOALHRLTLTKNYLSRTC 576
 RESULT 13
 BIRF_MOUSE STANDARD: PRT: 1403 AA.
 ID BIRF_MOUSE Q8R016: Q8R029, P81703: 009122: 009121:
 AC Q8R016: Q8R029, P81703: 009122: 009121:
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1E (NEURONAL APOPTOSIS
 GN INHIBITOR PROTEIN 5)
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99431676; PubMed=10501978;
 RA Huang S., Schaff J.M., Gromney J.D., Endrizzi M.G., Dietrich W.F.;
 RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
 RT functional transcripts." (1999).
 RL Mamm. Genome 10:1032-1035(1999).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=128/SV;
 RA Endrizzi M., Huang S., Schaff J.M., Kelter A.R., Wirth B.,
 RA Kunkel L.M., Miller W., Dietrich W.F.;
 RT "Comparative sequence analysis of the mouse and human Nalp5/MA
 RT interval." (1999).
 RL Genomics 60:137-151(1999).
 RN 131
 RP SEQUENCE OF 82-168 FROM N.A.
 RC STRAIN=129/SV;
 RA MEDLINE=97131520; PubMed=8975718;
 RA Schaff J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
 RA Kunkel L.M., Dietrich W.F.;
 RT "The mouse region syntenic for human spinal muscular atrophy lies
 RT within the Nalp critical interval and contains multiple copies of
 RT exon 5." (1999).
 RL Genomics 38:405-417(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -----
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 CC -----
 DB EMBL: AF135492; AAD56764.1; -;
 DB EMBL: AF131205; AAD56760.1; -;
 DB EMBL: U66326; AAC52974.1; -;
 DB MGD: MGI:1298220; Bircle.
 DB InterPro: IPR001370; BIR.
 DB Pfam: PF00653; BIR; 3.
 DB SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.

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DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1F (NEURONAL APOPTOSIS
DE INHIBITORY PROTEIN 6)
GN BIRCP OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SOURCE FROM N.A.
RP MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Gowney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
[2]
RP SOURCE OF 82-168 FROM N.A.
RP STRAIN=128/5VJ; PubMed=8975718;
RX Schorf J.M., Dameron D., Pritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the lgln1 critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
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CC
CC EMBL: AF242433; AAC82751.1;
CC MBL: U66327; AAC52975.1;
CC MGD: MGI:128822; Birc1f.
CC InterPro: IPR001370; BIR.
CC Pfam: PF00653; BIR_3.
CC DR SMART: SM00238; BIR_3.
CC PROSITE: PS01282; BIR_REPEAT_1; 2.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC APOPTOSIS: Regoat; Multigene family.
CC REPEAT 159 127 BIR 1.
CC REPEAT 159 127 BIR 2.
CC REPEAT 278 345 BIR 3.
CC SIGNALS
CC SEQUENCE 1403 AA; 159823 MW; 9D491250338C4F9 CMC64;

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OY 232 SAGFYVGRNDVKGRCGCGGLCKMGSGDDPWVLEAKKPPRCPELLRMKGO -EVYDEIG 350
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 RAFFETGRKNDYKPCSCGGLCKMGSGDDPWVLEAKKPPRCPELLRMKGO 360
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 351 RYTHILLEDDLSSTDTGGEKND-----PPIYRPGP-----SSSDA----- 368
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 QY-----ALPEATETTESNDAAVSHVTVLGRSAQHPDARSLSQGLKDYRTS 415
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 369 -VWANNPVVSALE-----KEPNDDLYKTPYQSTI-----TTGNYKTYNDVYSALMAE 440
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 416 FCHMNLPEVCSGLDTHGDSVTSIKSHVQVYGALTPVFNLSVSWCYEGHAGSG 475
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 441 KREERKQAEWASDLSLRKRNALFOQLTCVPTLDMLKANYINNOEDIRKRT 500
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 476 KTFELK-RIAFLWASCCPLRYRQLYVLSLSIFP--DQGL-ANILCTD----- 522
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 501 QPLDARRELDITLYKGAANAIFKRL-KEIDSTLYKNLFYOKMKYTPEDVSGI-SL 558
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 523 -----LGNQGCISEY-----GLSSIQQLQDHYAFD-----LDYISGLSL 559
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 559 EQGLRDE-----RVC 571
OY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 560 FQALHTLYKMLPFC 576

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RESULT 14
BIR_MOUSE STANDARD: PRT: 1402 AA.
ID BIR_MOUSE
AC 950183;
PF 20 AUG 2001 (Rel. 40. Created)
DT 20 AUG 2001 (Rel. 40. Last sequence update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1F (NEURONAL APOPTOSIS
DE INHIBITORY PROTEIN 7).
GN BIRCP OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SOURCE FROM N.A.
RP MEDLINE=2041747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Gowney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC
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CC
CC EMBL: AF242433; AAC82749.1;
CC MBL: MGI:1858256; Birc1g.
CC MGD: MGI:1858256; Birc1g.
CC InterPro: IPR001370; BIR.
CC Pfam: PF00653; BIR_3.
CC DR SMART: SM00238; BIR_3.
CC PROSITE: PS01282; BIR_REPEAT_1; 2.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC APOPTOSIS: Regoat; Multigene family.
CC REPEAT 159 127 BIR 1.
CC REPEAT 159 127 BIR 2.
CC REPEAT 278 345 BIR 3.
CC SIGNALS
CC SEQUENCE 1402 AA; 159662 MW; CLDFPBA35983BOD CMC64;

```

Query Match 15.2%; Score 498.5; DB 1; Length 1402;

Best Local Similarity 26.9%; Pred. No. 1.2e-25;
Matches 167; Conservative 69; Mismatches 217; Indels 167; Gaps 23;

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OY 33 NSNNKKKDDSC-----LYMSYVSTPACVAVSESLAAGFYTTVDKDKCC 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 43 IKEMIMKKGNSQMSSEAKRLKTFSSYDTRFSWTP---QEMAAAGFYHTVKRLGVCFC 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 86 CGLMNDNMKLDSPDKKOLYPCSCFSTIONVVSAGTSKNTSPRNSFAHSLPTLEH 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 100 CSLTIGNSLKLRIERHKRLRPECPLD--GKQVNGIKGYDIRVK----- 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 146 SLSFGSYSSVSPPLNSHAWEDISSRTNPSYAASTEARFLTYHMMPLTF--LSPEE 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 -----SPEKM-----LROCKARY--HEEERKLESEDEMPRYAGCTSPAV 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 204 LARAGFYITGPDVAVCFACGSKLSMWEFKDAMSEHRHNPCLLEN--SLETLRFST 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 LSAAGFYVFKRDIYVCFSCGSLGKWEEDGDPWKHAKMFKCEFLSKSSSEIADYI 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 262 SNLSMOTNAA-----SMRTFYWSSVVPYOEOLA 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 OGYSGEVATGHEHFKSVWRELPRVAVCNDVSFANEELMDMFMDPQESPVEALV 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 292 SAGFYVGNNDVYKCCDGLRCWESGDDPWVHAKWPKCFLLRMKGQ--EPVDEIIG 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 RAGFYTGKDIYVCFSCGSLGKWEEDGDPWKHAKMFKCEFLSKSSSEIADYI 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 351 RYHMLEOLLSPTTGEEN-ADPPIIH-----FGGSSSEDA----- 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 QI-----ALPETETRESNMGDAVAHSTVAVDIGNSEAMFOPARSLSEQLRDYTKTS 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 389 -VWAKNPVYKAL-----EMGFNDLYKOTVOSKILTFGENYKTVNDIVSALLNAD 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 416 RCHNAPGCSLGTDLHLSCVYSISKHSIPVQK-ALITPEVFNLSVWCEGAS 474
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 440 EKREKEKQAEEMASDLSLRNNMALFQOLTCVLP--LDNLKANVINKOEHDITK 497
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 475 GKTFEUK-RIAFLWASCCPILTYFDVYLSLSTIPQGDIIITCOLL----- 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 498 OKTQPLQARELDTIIVKGNMAANIFKNC-KEIDSTIKNLFVOKNKKITPEVSG 556
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 525 -----GNGCISEVCLSSISQIOLDRQVLP-----LDIYSOL 556
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 557 -SLEEDRLDEE-----KTC 571
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 557 ASLPQALHTLITKNTLFRIC 576
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15
IAP1.DROME STANDARD: PRT: 438 AA.
AC 024306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE APOPTOSIS 1 INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD PROTEIN)
GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye, imaginal disk;
RA MEDLINE=66128128; PubMed=8548811;
RA Hay B.A., Wasserman D.A., Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins function to block cell death."
RL Cell 83:1253-1262(1995).
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND HID-DEPENDENT CELL DEATH IN THE EYE.

```

CC -I- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -I- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC
DB EMBL: L49440; AAC41609.1;
DB Flybase: FBgn003691; th.
DB InterPro: IPR001370; BIR.
DB Pfam: PF00653; BIR; 2.
DB Pfam: PF00997; zf-C3HC4; 1.
DB SMART: SM00238; BIR; 2.
DB SMART: SM00184; RING; 1.
DB PROSITE: PS01282; BIR_REPEAT_1; 2.
DB PROSITE: PS01443; BIR_REPEAT_2; 2.
DB Apoptosis; Zinc-finger; Repeat.
FT REPEAT 44 110 BIR 1.
FT REPEAT 226 293 BIR 2.
FT ZN_FING 391 425 RING-TYPE.
SQ SEQUENCE 438 AA; 48098 MW; A6C22C8D5AEF29 CRC64;

```

Query Match 14.8%; Score 484; DB 1; Length 438;
Best Local Similarity 22.6%; Pred. No. 2.3e-25;
Matches 126; Conservative 62; Mismatches 128; Indels 242; Gaps 12;

```

OY 162 NSRAVE---DISSRTNPSYAASTEARFLTYHMMPLTFSESLAAGFYTIGPGR 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 22 NNNTQFLFNKLNKTRND---LAREEFLKTLTQWPLDWRQLQAGTQMTYTAGSK 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 218 VACFACGSKLSMWEFKDAMSEHRHNPCKP-----LENSLETFEST- 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 VACFGEVATGHEHFKSVWRELPRVAVCNDVSFANEELMDMFMDPQESPVEALV 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 262 -----SNLSMOTNAA-----SMRTFYWSSVVPYOEOLA 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 GANDSTLEKHEATVABGVTPMSQLIOSIGHAVNAGSTGAAPRVYATPASTAQ 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 271 -----ARRTFYWSSVVPYOEOLASAGFYTIGR 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 198 ANGVOPETGPRASAGNTFFQVETATETATKTFEAMPRMLQKPHLAAGEFTYGV 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 301 NDVYKCCDGLRCWESGDDPWVHAKWPKCFLLRMKGQ--EPVDEIIG 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 258 GBRVYKSCGSLGKWEEDGDPWKHAKMFKCEFLSKSSSEIADYI 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 361 SISDPTGEMADPILTHFGGSSSEDAVMNNTYVKSALMEGNLDLYKOTQSKILTT 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 317 ESTISGID-----TVAS----- 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 421 GENKRYNDIVSALLNMEDEKHEEKOAEEMASDLSLRNNMALFQOLTCVLPILD 480
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 -----TQASEEDQSTLSSEBAVSQDA-----PEVAP--- 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 481 NLKANVINKOEHDITKQTPQLQARELDTIIVKGNMAANIFKNCLEKIDSTIKNLF 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 357 -----TAVRRI-----NKI 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 541 VOKNKKITPEVSGLSLEQLRLQDEBETGKCMKGEVVFIPGHLVYGCOPASIR 600
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 367 VAVAAVAVTSSNGST-----SIREPLKCTICGAYINAFIPGHVYVACASVY 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 601 KCPICRIGIKGVTFEIS 618
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 421 KCPICRIPPTDVHRYVS 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: January 7, 2002, 16:05:23
Job time: 1402 sec
